

Sa247851_0026.Dna
Gcg_Geneseq_D:T19113

XP2128459

ID T19113 standard; cDNA to mRNA; 351 BP.
AC T19113;
DT 04-JUL-1996 (first entry)

DE Human gene signature HUMGS00127.
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
OS Homo sapiens.
PN WO 9514772-A1.
PD 01-JUN-1995.
PF 11-NOV-1994; 94WO-JP01916.
PR 12-NOV-1993; 93JP-0355504.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI; 1995-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human

PT tissues
PS Claim 1; Page 304; 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 351 BP; 123 A; 45 C; 58 G; 121 T; 4 other;

SCORES Init1: 1638 Initn: 1638 Opt: 1706 z-score: 597.6 E(): 5.9e-24
98.9% identity in 349 bp overlap

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      1480      1490      1500      1510      1520      1530
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              |||||
T19113              GATCACATTATNATAAATAAATGAAAAAAT
                      10      20      30

      1540      1550      1560      1570      1580      1590
Sa247851_002 GATTTAATCTGTAATAAACTGGTTTATTGTGCAGTGACTGTAATATACTAGAGTTATAAT
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T19113              GATTTAATCTGTAATAAACTGGTTTATTGTGCAGTGACTGTAATATACTAGAGTTATAAT
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40 50 60 70 80 90

1600 1610 1620 1630 1640 1650
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100 110 120 130 140 150

1660 1670 1680 1690 1700 1710
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160 170 180 190 200 210

1720 1730 1740 1750 1760 1770
Sa247851_002 GAGAGCTGTTATCCTAACTGATTAGTATGTTCTGTAATTGAGAAAATGTTACCAAATT
T19113 GAGAGCTGTTATCCTAACTGATTAGTATGTTCTGTAATTGAGAAAATGTTACCAAATN
220 230 240 250 260 270

1780 1790 1800 1810 1820 1830
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T19113 ATACTTTTTAGTGATTTACATGTACATTTTATAGGGGACATGTTCTGTGTATAGCGAATA
280 290 300 310 320 330

1840 1850 1860 1870
Sa247851_002 AATAACTTTTATAGTATCAAAAAAAAAAAAAAAAAA
T19113 AATAACTTTTATAGTATCACN
340 350



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(71) Applicant: Matsubara, Kenichi
Room 804, 18-1, Yamadahi-gashi 3-chome
Suita-shi,
Osaka 565 (JP)
Applicant: Okubo, Kousaku
11-26, Segawa 2-chome
Minoo-shi,
Osaka 562 (JP)

(72) Inventor: Matsubara, Kenichi
Room 804, 18-1, Yamadahi-gashi 3-chome
Suita-shi,
Osaka 565 (JP)
Inventor: Okubo, Kousaku
11-26, Segawa 2-chome
Minoo-shi,
Osaka 562 (JP)

(74) Representative: Vossius, Tilman et al
Dr. Volker Vossius,
Patent- und Rechtsanwaltskanzlei,
Holbeinstrasse 5
D-81679 München (DE)

(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

EP 0 679 716 A1

[illegible]

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

SEQ ID NO:7844
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

SEQ ID NO:7845
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

SEQ ID NO:7846
 SEQUENCE LENGTH:38
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

SEQ ID NO:7847
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CCAGGGTTTT CCCAGTCACG AC 22

SEQ ID NO:7848
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 TCACACAGGA AACAGCTATG AC 22

50 Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1

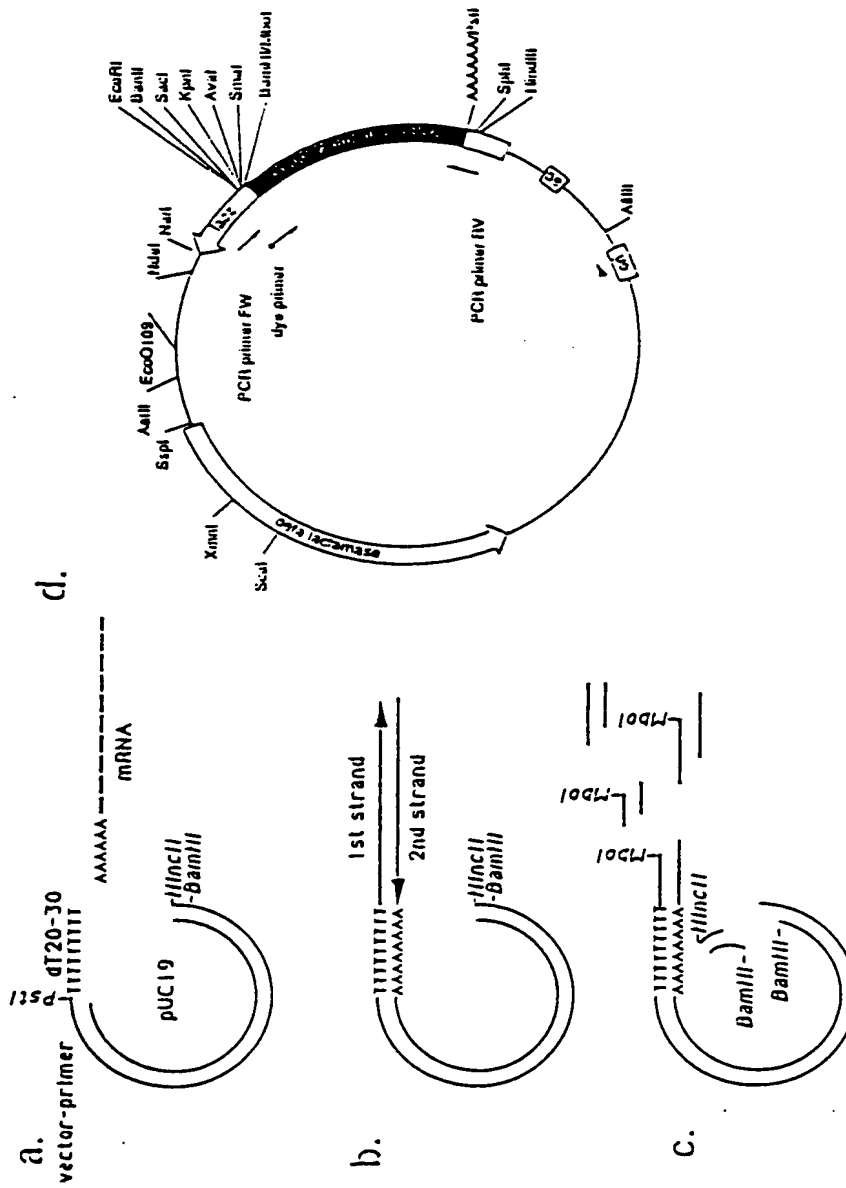


Fig. 2

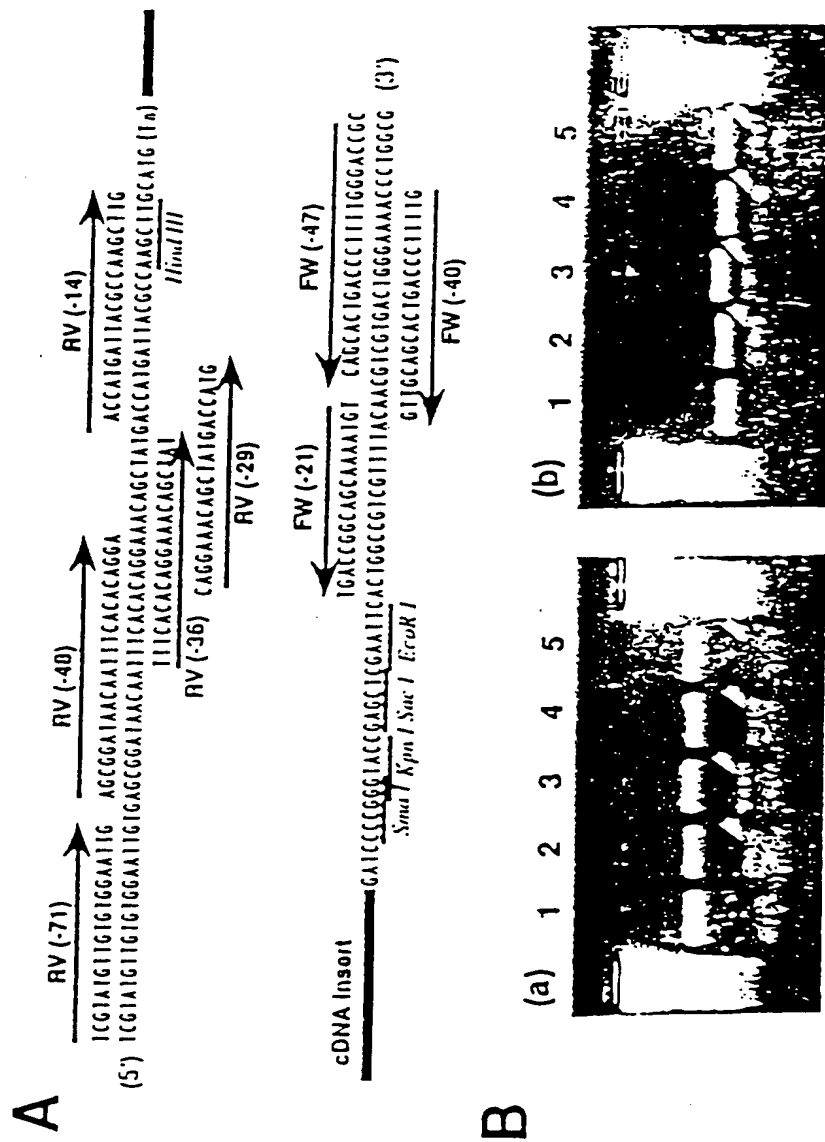


Fig. 3

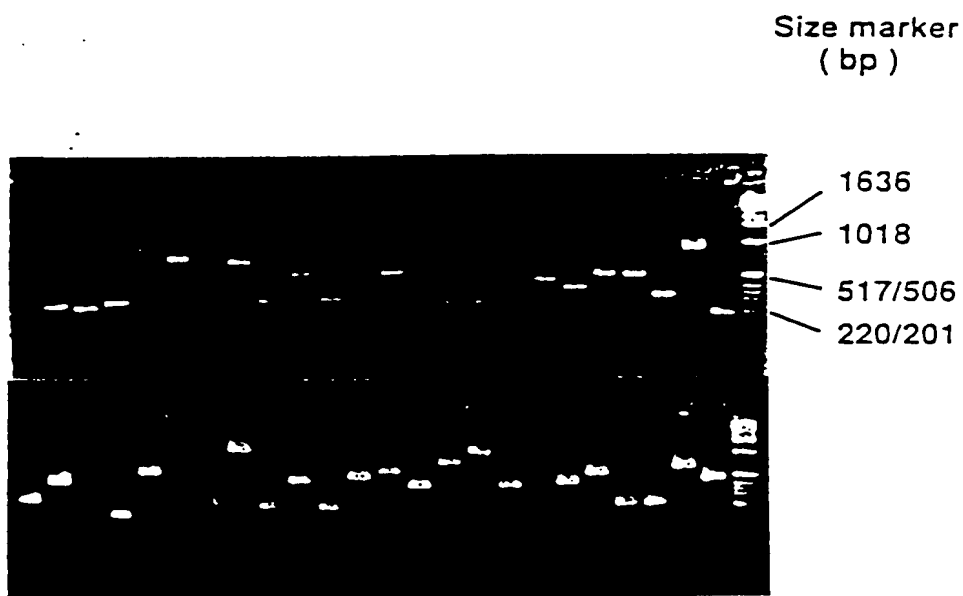


Fig. 4

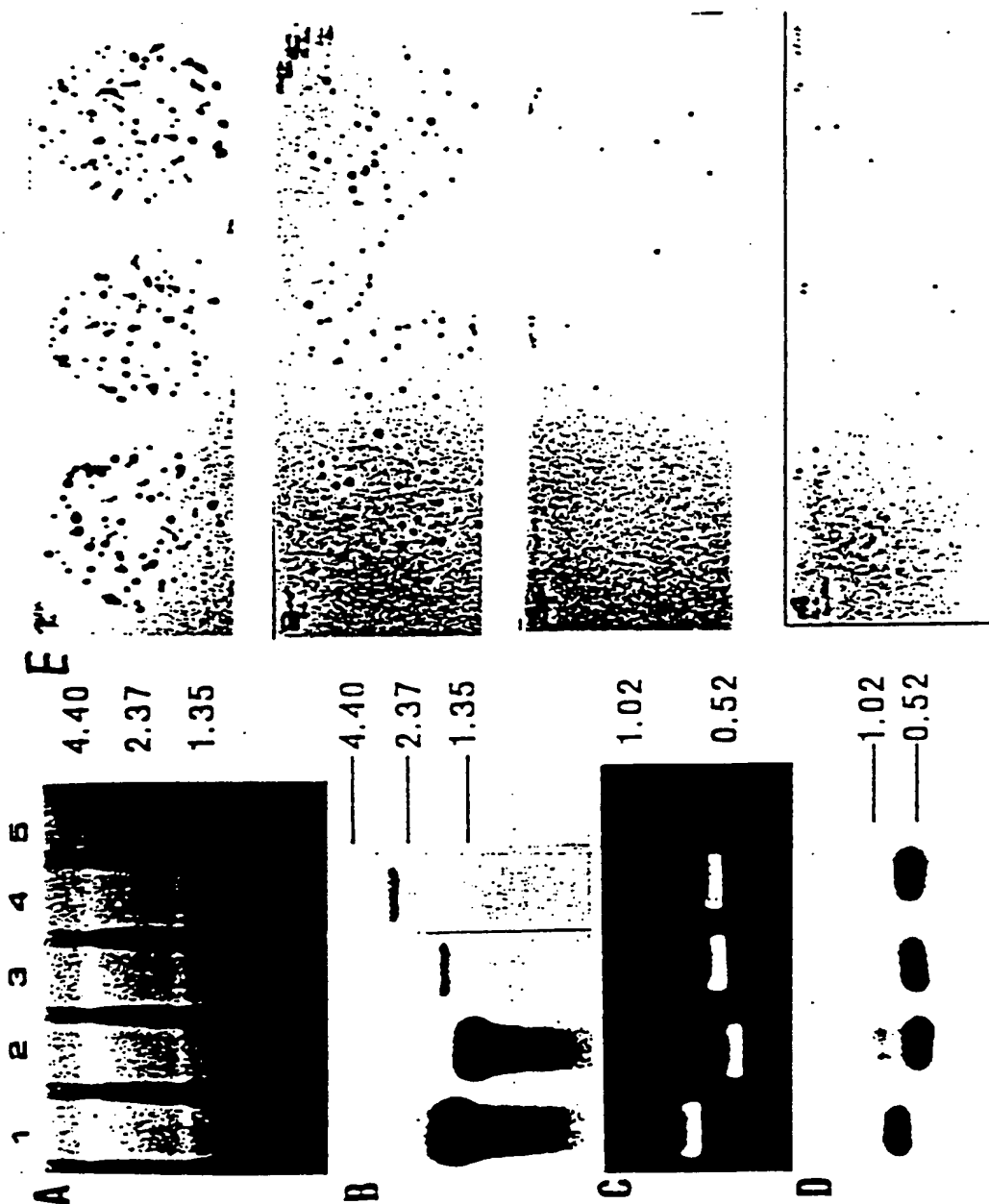


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-andrypsin	HnRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b)x10	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A			B			C		
			in 902 (%)			"in 8,000 (%)"			"in 26,400 (%)"		
I	a15	Elongation factor - 1A α	22 (2.2)			307 (3.5)			NT		
	c321	Translationally restricted tumor protein	12 (1.2)			89 (1.0)			NT		
	lb030	α -1-antitrypsin	8 (0.8)			119 (1.4)			NT		
	hm01b02	Light chain of ferritin	6 (0.6)			62 (0.7)			NT		
	c13a04	NADP(II) Menadione oxidoreductase	4 (0.4)			27 (0.3)			NT		
	hm02d02	Ribosomal protein S11	3 (0.3)			29 (0.3)			NT		
	lb042	Human RNP core protein A1	2 (0.2)			7 (0.1)			NT		
	s155	unknown	1								
II	s159	unknown	1			2			5 (0.02)		
	s639	unknown	1			2			4 (0.02)		
	s635	unknown	1			1			3 (0.01)		
	s170	unknown	1			0			2 (0.01)		
	s154	unknown	1			0			1 (0.004)		
	s167	unknown	1			0			1 (0.004)		
	s645	unknown	1			0			1 (0.004)		
	s647	unknown	1			0			1 (0.004)		
	s632	unknown	1			0			0 (<0.004)		
			1			0			0 (<0.004)		

Sequences of primers													
GS	Cil	Chromosomal position	Sense		Anti-sense		AT	IIQ	IIE	MIO	CO	G	T
			Sense	Anti-sense									
91001748	pml2366	1	CAGAGCCCGAGTACACTAT	AAGTTATGTGTGGGTGAC	48	114	115	104	110	1	2		
91001076	pml2444	1	ATGGGACAGTTACACTTGA	CCAGCTTCTCTGACTTGAGA	48	83	81	>200	>200	1	1		
91001075	pml0883	1	TGGACTGTGGATACCTATCT	ACAGTACCCCTGAATGGCT	48	124	124	103	107	4	4		
91001047	pml1772	1	GTCACTGTACGCCATAGCAC	ACCATCTTCAGCCACACACT	50	104	104	180	>200	6	6		
91001094	pml0347	1	GCCCCATACAGGAACTC	TAATTTCCCATCCCGTAAAC	51	114	116	>200	200	1	1		
91001116	pml1771	1	GGGTTTCATAGGGGTAGACC	GCCCCAATCTGTCAAACTG	49	95	95	78	107	1	1		
91001191	pml0609	1	TTGCTGGATTGTAACTTTG	GGCTGAACATTCACCTCTTG	47	97	97	200	200	1	1		
91001200	pml1351	1	TTAGAGAGACCTTATGGAGACC	AATATCTGGTTAGTCACITAC	47	97	98	200	200	1	1		
91001346	pml0982	1	TCAGGTCTGCTGGAGGATG	AATCTACAGACAGTATTTG	53	120	122	>200	>200	1	1		
91001446	pml1518	1	AAGGTGTACAGGATATTGCAGA	TGCAATAGCCCAATCTCAT	47	130	125	>200	>200	1	1		
91001464	pml1439	1	CCAAAGACTCCGTTGAAACA	TTTGGAGAGCCATAGACAG	51	100	100	>200	200	1	1		
91001468	pml0427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACCAATTTCTTA	40	98	98	200	200	2	2		
91001521	pml2785	1	CCCAATCAAAATTTTAAATG	TTTGAATCAGACACATGAAGTT	43	102,115	100	>200	>200	1	1		
91001554	pml2291	1	CCAGAGAGTTCAGGGGATG	GGTACAAAGTGCMAATGACT	46	57	57	78	155	1	1		
91001572	pml2006	1	CCACATCTGGTCTAGCACCTG	AACTTTATGCGAGTCTCT	44	58	53	>200	>200	4	4		
91001720	pml1350	2	CATGATACTCTCGGTGGTA	AAACAGTAGTTGCCAGCACT	46	84	108	200	200	1	1		
91001036	pml1730	2	AGGCTGAATGTGGCATGCT	CCGTTATGTGTACATGCTCT	48	119	119	93	115	1	1		
91001081	pml0931	2	AAAGCAATACAAATACCAA	TTCAATATGTTTACCAGTA	40	90	90	200	200	1	1		
91001090	pml0925	2	TAATGTACACAGATGAATAG	TATGTAATATGCGAGTAA	45	88	88	200	200	1	1		
91001213	pml2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGAAATCAACAG	47	125	125	150	>200	1	1		
91001252	pml0935	2	TCGAGTTTGTCTCTAATA	GGAATATCGCTTCAGTTG	43	103	103	200	200	1	1		
91001268	pml2093	2	AGTCCCTCTGGCTCCTCAT	TATCGTCAGTGGCTTTATG	52	137	137	>200	200	1	1		
91001438	pml2435	2	TTTGTACCTACGTAGAGTACTT	ATCCGTGCCACACATAGTGA	45	105	108	200	200	1	2		
91001442	pml1671	2	TTATAGGAGTCAATATCTGTG	AGTCCCATCTTCCACATG	45	67	65	>200	>200	1	2		
91001453	pml1245	2	TTGCTTCCCGTCTCTAAGT	ATGTACAATTTGGTATGTAGG	45	75	75	170	190	1	1		
91001535	pml1246	2	ATCTACTTTGTGTGAAGTG	ACTGATTTTGGTCCCATCTG	44	68	67	200	200	1	1		
91000675	pml0449	3	CGAACATTCACCTCTCAT	ATGATTTATTAAGGCAAGAA	43	68	63	200	200	3	6		
91001001	pml1758	3	TCGGCTCTTTGGTGTGGA	GGCCCACTGATACAAATGTC	51	115	115	200	200	1	1		
91001218	pml2434	3	AAAGAAAGCACACTGCCTAA	ATGTATAGACAATCCAAAG	42	90	90	200	200	1	1		
91001219	pml0668	3	GTAGTCTCTGCCCTTAGC	AAGGATTTGATTTCTACAT	43	77	77	200	200	1	1		
91001277	pml1729	3	GGTCCGTTTATTTGACAT	AACAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1		
91001306	pml1022	3	GATCGTTGGTGTAGTTCAGTC	CTGCAAAATACAGGGAATCAT	46	83	83	160	140	1	1		
91001418	pml2209	3	ACCCAGTCCCAATCCAGT	ACACTCCCGCCGCTTACT	55	105	105	113	>200	1	1		
91001466	pml2455	3	ATCAGCTGGCTGTAGTAT	TTAAGAGATGAATTTATGGT	42	130	130	190	>200	1	1		
91000271	pml1252	4	GTCTTCTGCTATCTGTCTA	AAGCAATTTATTCAGGCTTAA	43	90	90	95	>200	1	3		

Fig. 7

91000148	pm2256	4	GGCCAAAGTTCTCTAGTAT	GTTCAGTTTATTCAGAGCA	42	62	62	62	62	69	1	2
91001052	pm1151	4	GTGCCATGCACTGTGTAT	GTCCATATTCATCATCA	43	80	80	80	80	-	1	1
91001215	pm0908	4	AGAAATTAATAGCATAGGT	TAGAGTCAAAAGTTCCTG	43	100	100	100	100	130	1	1
91001298	pm2367	4	ATCAAGTTTAATTCGTCA	CATCCCATCATACAGTC	43	116	116	116	116	180	1	1
91000993	pm0904	5	TCTCGTGAAGAGCAGCACA	TCTAAAGGAAGAACAGTC	49	101	102	102	102	200	1	1
91000998	pm1809	5	AAGCAATGCCCTATCCACAG	CTAAGAGCTTGACCCCTTCAT	45	87	87	87	87	>200	1	1
91001085	pm0319	5	TCACCACGATATTACAGT	GAGACATAGCAGGTAAAT	44	120	120	120	120	-	1	1
91001101	pm2364	5	TTACCTTACCGTGTCTTAC	AGACAAATATCCAAAGC	47	89	89	89	89	100	1	1
91001161	pm1160	5	ATTGTGATGGTTTACTA	AGAAATGGATGCTTTATTC	43	101	99	99	99	>200	1	1
91000053	pm2720	6	AATGTCATAGTCTCCTTCA	TGCATCTCAATGCTCTCT	44	78	78	78	72	>200	2	3
91001326	pm1154	6	CATTGAGACAGCAGCAGAG	CCTGGCCCTCTCTCTAGTA	53	102	104	104	145	200	1	1
91001334	pm1216	6	TAGGCAAAACAGAGAGAG	AAGGAGCTGGTGCAGGTTG	48	65	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCG	TCTAATATCTGGTCCCTTATCT	46	90	>200	90	>200	>200	1	1
91001523	pm0285	6	TTGTACGCTGTGCTCAGT	TTTAAATGTCATGGTAAT	42	86	70	>200	100	100	1	1
91001525	pm0328	6	GCACCTAAGCCTCCCAAGT	TTTATATCAGTCCCAAGC	49	138	138	138	>200	>200	1	1
91001582	pm2619	6	TCTGCATGACAGGACCAC	TTTGAGATTTATGATGATTC	43	62	62	62	>200	45	1	1
91000624	pm0991	7	GACCTGAAGTGTGAATGAT	AACCTAGCTATGCGGATTT	45	119	119	119	>200	-	1	2
91001145	pm0281	7	-AGCCAACTCGGGTCACT	CCACGGACAGGTGAGTCAT	56	159	159	159	115	>200	4	4
91001469	pm0219	7	AATCATTGGCGAGACTGA	AGACAAGTATATCCAGACA	45	88	88	88	130	-	1	1
91001579	pm1102	7	TCAGGCAGTCTCTCAGATA	TTTCCAGTATATCTGTTTA	44	77	76	76	170	-	1	1
91001707	pm0956	8	ACAGATATGCGTTGCAGACTAG	TCCATTAAAGCCAGCTCAG	47	81	81	81	105	70	1	1
91001176	pm2527	9	TGCGCTTAATGGTGTCTAC	AAACCCACACACACTAAG	48	99	99	99	118	180	1	1
91001248	pm2708	9	TGTATGGATTGGATTCTC	CAAAAGCAAAACAGCAGATA	44	95	95	95	-	85	1	1
91000260	pm0995	9	TTGCCATCAMAACACATACA	CTTGTGAGTTTGTGTTCTG	43	55	55	55	-	-	1	1
91001055	pm0959	9	TTAAGAAATCACCCTCATG	CACATGCTTATGGAACT	44	74	74	74	72	73	1	1
91001157	pm0547	10	AAGTATTTGCAAGATGTA	AAGAAAGACTGCTTGTGG	45	138	139	139	>200	>200	2	3
91001288	pm2245	10	TGTGAATGCTATCTCTCT	GCAATCGTTCCATATCAGT	47	100	100	100	200	>200	1	1
91000228	pm2664	11	ATCAAAACAAACATCCAGA	ACTATATATCTGCCAAGT	42	117	121	121	134	95	2	2
91001159	pm0800	11	GAATAGCTTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	100	84	95	1	1
91001315	pm0445	11	AAAGTGACCTTGAGACAGTGG	TCGAGCCAAATATACCTGACT	50	153	153	153	>200	160	1	2
91001352	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCATGGTTGAGAGCTA	47	83	85	85	-	-	2	2
91001469	pm0559	11	AACCCCTCTAGTAAGGCATTG	TTATTAACCAATCCAGTA	37	47	47	47	125	53	1	1
91001570	pm2810	11	CTGTAAAGGTTTTTGGATTATGT	TTTCATTTTCTACCAAGTTTAT	42	75	82	75	145	>200	3	3
91001266	pm0266	12	AGTGATGGAAGACCTTGAG	GTTCATTGAACGGTGTAGC	48	130	130	130	103	>200	1	2
91001163	pm2356	12	TCTCCCTATTCCACAGCAGT	AATGATTGCTAGGATAGCA	49	88	89	89	>200	120	1	2
91001193	pm1193	12	CACAGCATAAAGATCATATA	ACCTAAITTAGTTTCTCAC	46	100	100	100	-	-	1	1
91001235	pm2790	12	CATCATGCTACAGTCAGAG	CAGTTTGTCAAAATGTATTG	44	83	82	82	93	87	1	1
91001274	pm1355	12	AGATGTCAGTATCTCTCATGG	GAGAACAGCAGTAAGCAACCCAC	47	87	87	87	>200	>200	1	1
91001308	pm0368	12	CCAAGTCTAGGGTTACAG	TTCAATAGACCTTGGGTTAC	47	95	165	95	>200	>200	1	1
91000159	pm2845	13	CTAAGATTAAATGGGATTCC	AGTTAGTGTATGGCAGAGGA	46	104	104	104	>200	-	1	2

Fig. 8

g1001014	pm1659	13	TTGTAGCCCTATCAGAGTCA	AGACAGAGTATGCCATCTA	44	109,200	109	>200	100	1
g1001290	pm1731	13	GCCTTCCTGCTGCTGGT	GCAGTTATCATGGCTATCTCC	50	122	122	>200	130	1
g1001262	pm0118	13	ACTGAATGGAAATAGTCT	TACATATCATGACATGTGA	40	61	61	95	103	1
g1001366	pm0364	13	TGCTTAGCTTCCCTGCTTA	GAGCATTCGTGCTGCTA	45	67	67	-	-	1
g1001389	pm2301	13	CATGACCTGCTCAGACAA	GCCTTACTTAATGCTGACC	51	100	100	100, >200	-	1
g1001492	pm0541	13	AAATGAATGTAATAGCACT	ATTATGTTACAGGGAGAT	41	72	72	-	74	1
g1001367	pm0141	14	GTTTAAGTTTGTATTGGG	CATTCACGCTTACATTTCT	41	77	77	>200	180	3
g1001564	pm2307	14	CGTTCCAAACTGTAATC	AATGCTCATTTATCTCAAG	42	55	55	>200	>200	1
g1001576	pm2019	14	ATCACATACCTTTAGTGG	ACGTAACATTTATGGAGAT	39	69	69	-	-	1
g1001339	pm2220	15	TCCCATCTCAGTGTAACT	TGAGAACAAAGGACCACT	47	70	70	80	150	1
g1000980	pm0985	16	TTGGAATGGAACTCTGCTA	ACTATGCTGCTGAAATGG	48	79	70	66	70	2
g1001242	pm1127	16	CCCTGTGTTTACATGTCA	TATTAAATGCTCCATTCAT	44	105	105	103	102	2
g1001516	pm2543	16	ACAGTGCTAAATCAAGGTG	TCTGACAGTCAAGGTGCAAT	45	70	70	>200	-	1
g1001566	pm0912	17	TTGTGTCGACTATGTAA	TCACCTTTAATGGGAACCAAG	41	53	53	>200	>200	1
g1000806	pm1157	17	CTGTCCATGTCTCTACAG	TAGAGGAGAACTGTGGTT	47	77	77	140	>200	2
g1001015	pm2369	17	ATATCAGCTTCCCATCCAT	TCAATAGGTCCTCTCAAGC	50	80	80	>200	>200	1
g1001156	pm0202	17	CAGAAATTAAGTCCAGCAAT	TGCTATGCTGCTTTAAGT	45	103	100	>200	>200	2
g1001172	pm2117	17	AAATCTGTGGTATTTCC	GTGATCTAGCTTACATGTC	41	118	118	145	200	1
g1001301	pm1078	17	TAAATTTGGAAATCTCTGGA	ACACATTTGGTITGCTTAAAC	47	100	100	95	97	1
g1001316	pm0514	17	TGTACAGCAGCAGCTTCAT	TGCTACATTTAATCCAGC	45	128	129	-	1	1
g1001356	pm0528	17	CATCTACAGCAGCAAGAAAC	ACCTAAGATCCAGAAAC	40	90	90	69	>200	1
g1001495	pm2212	17	TGACTGCAATAAGGATTTGT	GAACATACCACTTATTTCT	46	90	90	180	>200	1
g1001522	pm0642	17	GTCTTACGACGATTTGAGT	ACTTCTCTTGGAGGACACA	45	68	68	160	-	1
g1001074	pm1815	19	TGTGTCTCCAGCTTTGTAG	GTTACATTCCTTGGTACAG	49	65	65	>200	>200	1
g1001117	pm0289	19	GGATCAGACCAACAGTCTG	GCAGGTATTAACAGATTA	46	50	50	-	-	1
g1001467	pm1608	19	GAAGCCACCCCTGCACCTCA	GGAGATATGGGGAACCGGT	54	93	93	>200	>200	2
g1001069	pm1879	20	GCCATGCTGTGAAGTGATGT	TTAAGAGCCATAGCTAGGATA	48	140	140	-	-	1
g1001084	pm1146	20	GCCCTTAGGATTCAGTGGTC	ACCACCAAGGTCTTTCAGG	52	66	66	100	>200	1
g1001128	pm0112	20	TGCTGGATGACTCTACAGC	TCCCTATCATGGCTGCTGTT	49	59	59	59, 115	59	1
g1001132	pm0332	20	CTGCTCGGTAGTCTGACTC	CAATGGTCAAGAGACAT	49	135	135	153	160	1
g1001158	pm0647	20	TCTGATGATGATGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1
g1001210	pm1774	20	GGAGCCACATGGATGATTG	AAATGTACCCTGGCACCTC	52	124	124	>200	>200	1
g1001377	pm1235	20	AGCCATCTGGTATGTCTTA	GGAGCAGATGAACCTTCAC	44	90	90	>200	>200	1
g1001395	pm1701	20	TCCATGGTGTAGAGCCAG	CCACATCTCCCAACAGGAGT	54	142	142	>200	74	1
g1001427	pm2101	21	GTCAGCTCATGTCTACACAG	TTTATAGTGACACACAGAGT	45	130	130	180	>200	1
g1000374	pm0648	21	CTCTGCTATAAAGTAGAG	ACATTTGTTGCTAAATGA	39	50	50	145	>200	1
g1001444	pm0912	22	GGTGTAGTGAACCATTTAG	AGTTGCCCATCTCCGTGTC	46	124	124	>200	>200	1
g1001473	pm0911	22	GGCTGTGCTCCCATCTGT	AGAAAGCCCAAGTAGTCC	48	65, 80	65	100	125	1
g1001479	pm2231	22	TGAGCTGCACCTACCTGTGAGAG	AAGCAGGTGAGTGGGTTCCT	50	94	94	67	135	2
	pm2328	22	TACAGCCCTCCAGCTAAAC	TTTATTCGTGCTGCACACAC	46	65	65	190	>200	1

Fig. 9

91000999	pml759	X	CTCCATAGTTACCTGGATT	TCACCACCACTATTAGCA	47	103	103	-	-	1	1
91001149	pml2180	X	GGAGGGAGATATAGATTGT	AAAAATCCAGAGACTGA	46	70	70	135	150	1	1
91001161	pml0508	X	TTCATAGTGTACCAGTT	GGAGGATTGAGATACAT	40	85	85	>200	71	1	1
91001406	pml291	X	TATGCCAGTGAATGTTGGTAA	GTAAGGTTTATCTTGCATCAGA	47	82	82	>200	80	2	3
91001160	pml2289	1,16	ATCTGCTGAATACATCTG	GGGGAGAGACAACATGAC	46	70	70	68	130	1	1
91001436	pml0112	1,2,12,Y	GATCCGATGGGAGTGAAT	AATACAAAGCTAACCCAACT	44	69	69	170	-	1	1
91001404	pml2272	1,2,3,5,8,12,14,17,X	TGGAAATGACATCTCTAT	TTAATTTGAACAAAGCACT	43	130	130	150	132	2	2
91000360	pml0314	1,2,6,X	TATCAGCTGAATATGTCAC	TTACTGAATCCAGCCACCA	45	93	93	110	-	1	3
91000140	pml1481	1,3,4,5,8,16	TCCAAATGAAGAGGTGTA	AGTTGACAGCCAGGTGAATG	43	96	96	100	100	1	3
91001354	pml1561	2,20,21,22	GTCTGTCAAGCCAGATCA	TTTTATTTTGTCTCCAGT	43	110	110	170	150	1	1
91000336	pml2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATATGGTGTACACTCG	43	61	61	-	-	2	6
91001077	pml0943	2,5,14,C	GCCTGTATTTACCACTC	ATGTCCTTTGCTCCAGTTA	46	82	82	>200	82	1	1
91001192	pml1853	2,8,12	TCTGAGGACATCCAGACAG	CAGTCAAAACCAACCGTAT	49	95	95	93	160	1	1
91000213	pml1776	2,9,13,17,X	TGCATTAAGGGAAAGCCA	CCGTGTAGGTGATGAATG	49	78	80	>200	>200	1	2
91000919	pml0885	20,X	GTCAATTGATGCAATTC	ACATTTTATTTTCAACG	37	45	45	-	-	1	2
91001109	pml0457	3,10,15	CATGTACTCAGAGGCATTC	GCACATCAAAATCCCAACT	50	133	133	>200	150	2	2
91000071	pml2551	3,4,M	CAGGGACTGGAGCAGGAAG	GATTTACCCATAGGAAGC	50	101	101	101	88	3	3
91001426	pml2632	3,6	TTAGGAAATATGTTAGACAG	ATAGTATGGGTGACACAGTA	43	80	80	>200	120	1	1
91001391	pml1133	3,8	TGGATTGCTTACCTGTT	ACACCTCAGGAGATGTTAC	47	93	93	95	>200	1	1
91000377	pml2750	3,9,10,15	GCACACAAAGCCAAATCAGA	CTCTTACACCAACAGCAG	50	96	96	>200	125	2	10
91000605	pml0626	4,6	GGATTCTATTGCTGTCAAT	GTTTATGTACGGCATTTAC	44	105	100	>200	>200	2	4
91001212	pml1234	6,20	GCATTAACAGCAACAAATA	CTGTCCATGTGGCATAAACC	44	119	110	105	107	1	1
91001312	pml0606	7,18	AGATGCTACCATTAGGGATA	TTTAGACATACAGAGAGT	43	81	81	102	-	1	1
91001411	pml1253	9,11	CCAGACTACAGCCTGATGGC	CCCTACCCCAACAACCTCT	55	75,130	75	>200	>200	1	1
91001257	pml0115	9,M	ACCAATGTCACTGCTCTAAATA	CCCATATAGTGAAGAGGTAGTTC	48	125,155	127	125	>200	1	1
91001458	pml0126	10,15,22	AGCAATGTTTACTGGATT	TTCATCTGACTGGAGGAAAT	42	107	107	-	-	1	1
91000290	pml2703	10,15,22	ACTACCCCTGAGATATTAGTT	TTCATTTATTGATTAGTTGA	46	100	100	170	-	1	1
91000314	pml2643	11,M	ATACCATTCCCGTGTACCG	GAGGAGCTCTACTGGTCT	50	72	74	72	>200	3	20
91000403	pml2643	12,19	GCACCAGAGCAGTTCGAG	TGGGAATGAGAAAATAACT	46	83	83	81	-	1	1
91001487	pml2773	12,M	GATCTCAGTCTCGGTTTAT	TACATACAAAGATGCCAACAGT	44	80	80	79	68	1	1
91001275	pml2725	13,16	ATCTGTGTGCTGCTTTC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1	1
91000276	pml2780	14,16	AACCTGTTTACCCCATCTT	AGGTATTGTCCACCAGAA	48	87	87	>200	>200	1	1
91001435	pml1683	17,20,C	TGTTGGTTCACCATTAGAG	AGAACACACATCAAGATGC	46	90	90	>200	90	1	1
91000056	pml1740	17,22,Y	GAAATGCATCCAGACGTA	CTAGTTATATCTGGCTCTG	44	81	81	>200	200	1	1
91001393	pml0964	17,C	TTATCCCAAGCAGCACAC	TCCTCTCTCTGATGATA	49	120	120	>200	170	4	11
91000369	pml2217	17,C	ACTTAAGTAGCTTGTAGG	TGCCCTCTGCTGATGATA	43	95	95	>200	95	1	1
91001140	pml1213	18,C	CCCCAGTAAAGATTATTGT	AGTCAGGATGGAAGGATGA	44	92	92	-	92	1	1
91001217	pml1116	18,20	TGCAGATGATTTTCAGAG	CGTAGGTCATCTTTTCAGC	46	75	72	160	65	1	1
91001009	pml2824	19,22	ATCCCTGTGCTATTCAGAC	GCTCGTTAACCTACCTCAC	46	110	110	130	170	2	2
91001172	pml0887	19,22	GCCTGCATCTGTGTGACTT	AACCTCTGGGAACAATCAT	48	91	89	160	86	1	1

Fig. 10

91001057	pm12049	C	AGACACAAACACGCTAT	TTTTCTGATTATGACATGAC	45	75	75	101	75	1
91000173	pm1753	M	ATCTCTTGTAGCCATCTG	GTTAAGTCTGATGCCATT	42	64,100	64	64	>200	1
91001096	pm2236	M	GTAGAGTGCATTGACTAC	ACAGACAGGAATATCATC	42	100,96	110	110	112	1
91001166	pm506	N	GTCCACAGTCCAGCCTAAC	GCCACATATTAGAAATCATC	46	74	74	74	>200	1
91001151	pm2351	M	TGCTTTGTGGACTCTGCT	TTTACAGTCAATAMATACATGTT	44	110	110	110	106	1
91000229	pm2492	M1C	GCTAGAAAGAGGGCACTCA	CTTAACTGATAGCCAGCTC	46	75	75	75	75	1
91000245	pm2786	M1C	CACAAACAGCAACTTCAG	ATGGTTATTATCAGATTG	41	83	83	82	83	2
91000302	pm1701	M1C	TCCACCCAGAGAGCACACT	AATCATAGGAATAGGTTG	40	75,130	75	75	75	1
91000543	pm2318	M1C	TCGAGAAAGGACAAATCAC	GAACAGGGTTAGTCCATCG	48	50	50	58	58	1
91000675	pm1689	M1C	CATGAGCTACGGAAACAGG	AGCAGTCCGTGGGTCTGAG	51	81	84	84	84	4
91000732	pm1442	M1C	AAAGCATCTGAGAGGAACA	GGAGGACTCGCTGGGTCTTA	49	110, >200	110	110	110	1
91000995	pm268	M1C	GCAGCAGATACCTTTACACC	TGGTTCATTTCAGTCCCTTC	51	102	105	102	102	3
91001016	pm2783	M1C	GAAGCTTGTGAGGAAAGT	CAGACCCCATCTTTATACC	47	79	79	79	79	3
91001053	pm1144	M1C	ACGATATTATGATGATG	TCAAACCTTTATATATGCT	40	93	93	91	92	1
91001127	pm2290	M1C	AGATGAGTGTGGTCAGAGA	CCATCCGTGATCCAGTT	52	135	140	135	135	1
91001162	pm1626	M1C	ACTGGTGATGGAAGGTTACA	ECACACAGTGAGCCAGCT	47	55	55	55	55	1
91001216	pm2108	M1C	GAGAGCCCTGTCATCCTTA	CTCCCTTTGGTCTTTCTGT	49	100	100	100	100	1
91001253	pm1240	M1C	TAGTCAGGATTCAGTAAGT	ACATGATTTTGATATCTT	42	110	110	110	110	1
91001281	pm1131	M1C	AACTGGTCCATCAAGAGTG	AGTGAATAAACTCTCCACTCC	40	120	120	120	120	1
91001375	pm0952	M1C	ACTTAAACCCACCCAGCAT	ATCATGGCAGATGCAATAGAA	47	97	97	97	97	1
91001356	pm2216	M1C	ATCTGATGAGCTATATCT	CGTCTCTTTTATTTGACAT	51	89	89	89	150	1
91001411	pm0958	M1C	AAGAGGAGTTTCCCTGCTCA	GAGACCAAGGCACCTCTTA	45	100	108	108	108	1
91001460	pm2826	M1C	ATGGGTTTATCAGGGGTTTC	GGACATTTCTGTCATCTA	47	80	77	80	80	1
91001482	pm1210	M1C	ACATTTGAATGGGATGAGGT	GGACATTTCTGTCATCTA	51	75,55	75	75	75	1
91001493	pm0109	M1C	TTGTGACATTCCTTTTAGAA	CAGTCCCTGCTACTGAGACA	46	85	85	85	85	2
91001484	pm2042	M1C	GCCCACAGAGACATCATCT	TCTTAGTAGGTGCTCTGGTG	51	98	90	98	98	1
91000450	pm0304	No product	CAACACAGTACGCTGAAAGT	GAATATCTGTCATCTA	45	87	87	-	-	1
91000683	pm0808	No product	CTTTGGGATATTTTCTCAT	CCCTGGGTACTTTCTATG	43	60	60	62	-	1
91001255	pm1673	No product	AGCCAGCCTCTTGTATGTC	CTGGATTGATTTTCAATAG	44	87	87	-	112	1
91001373	pm2908	No product	TGTGGTATGAAATATCTGA	TTATGATGAGAGACACACT	43	98	90	163	>200	1
91001373	pm0361	No product	CAGTGTGCTTTGAAATG	TTATGTGAAATGTGGTTGT	41	63	63	-	150	3
91001526	pm0849	No product	TACAGCCGCTCTAAAGTC	TTTGAGCATCAAGGAAATCT	46	82	82	-	>200	1
91001574	pm1284	No product	TACATTCCTCAGACTCATCG	TTTCAAAACCTTTATCTT	40	86	86	>200	100	1
91001622	pm1606	No product	ATCAGAGCTCAGTTCCTGTAG	ATTTCCTCTTGCATGGTC	44	57	57	67	67	2
91001640	pm0852	No product	GATCTGAGCCCTAACTGGA	TTTGAGTTCAGCTTATTC	45	54	54	-	-	1
		No product	GATCTCTGTCCTTTTCA	TTTATACAGACACCATAC	36	45	45	-	-	1

Fig. 11

pm 2209 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y H M C N

Fig. 12

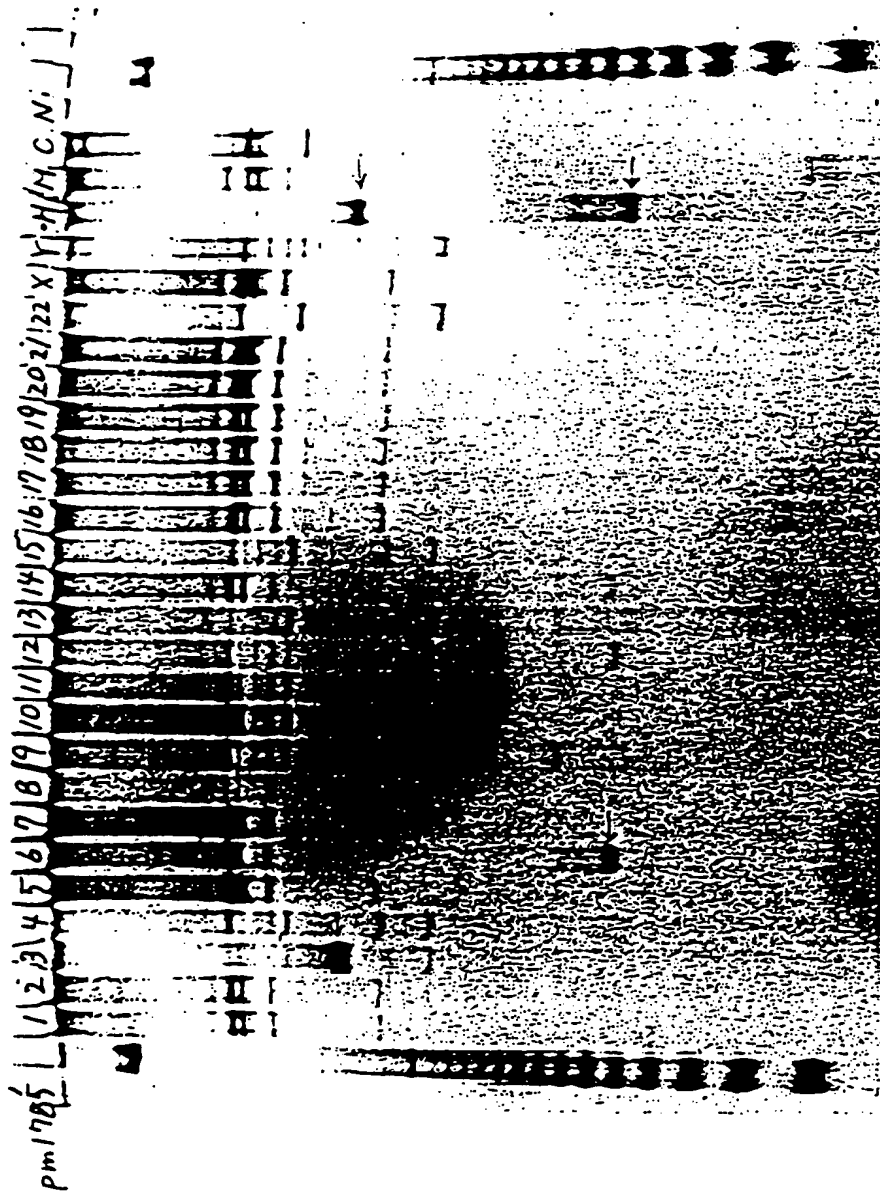


Fig. 13

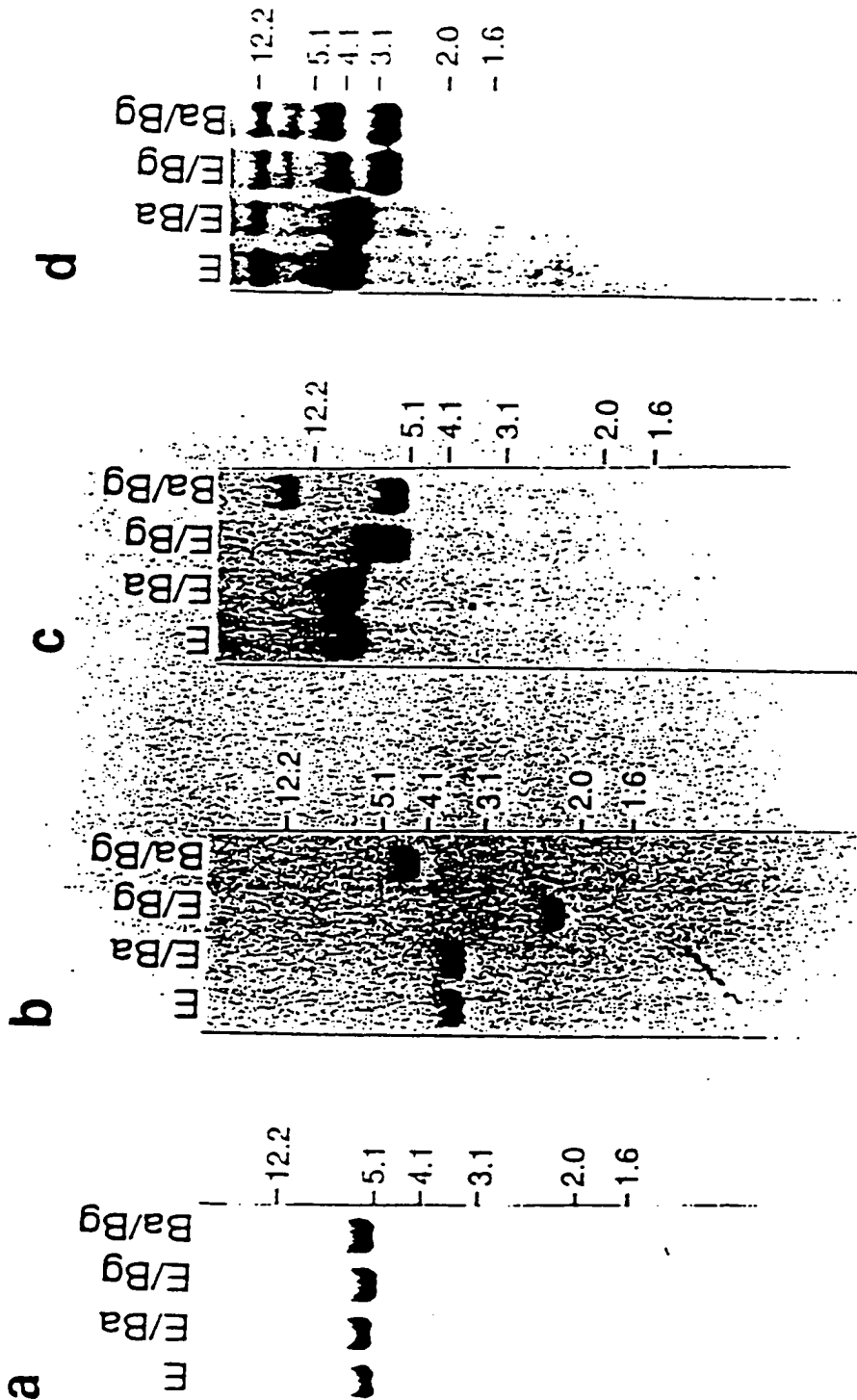


Fig. 14

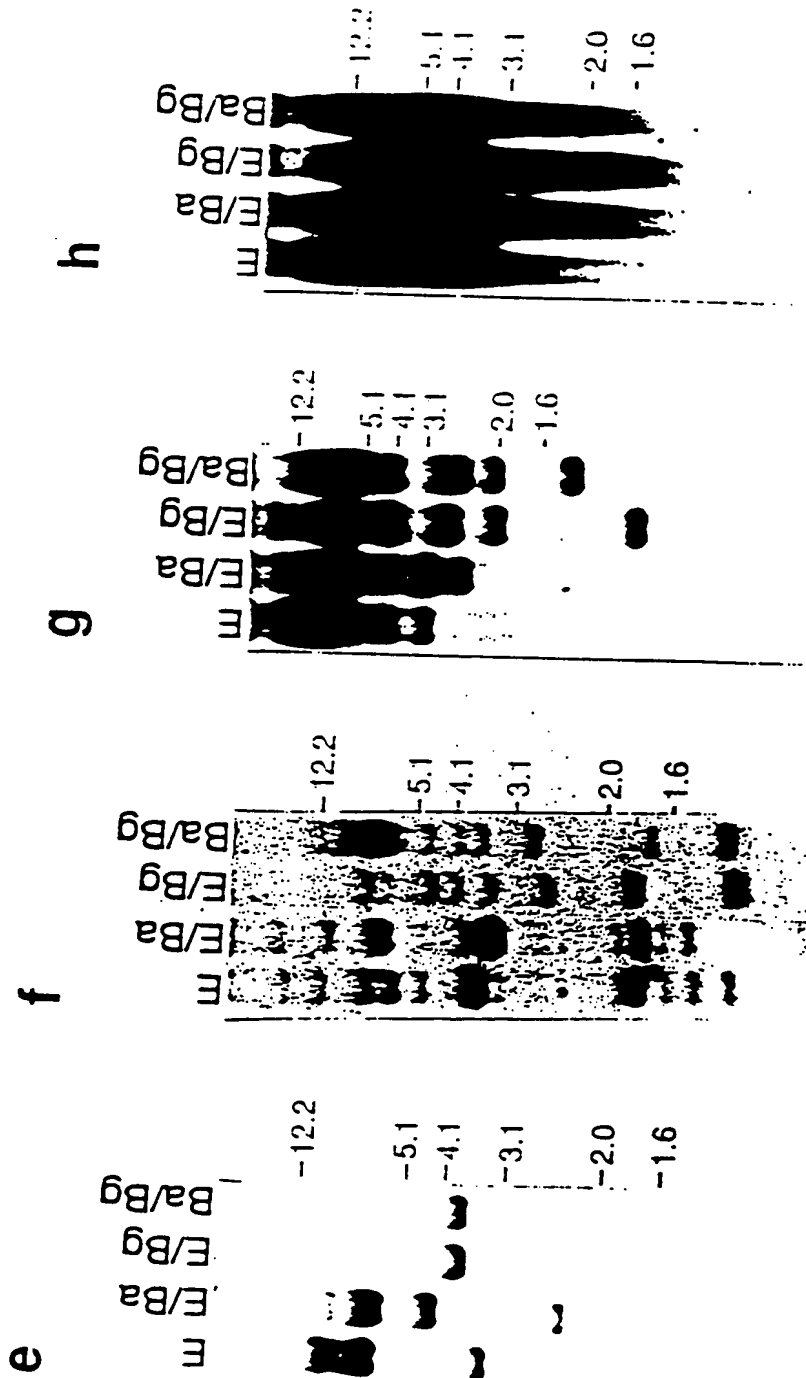


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

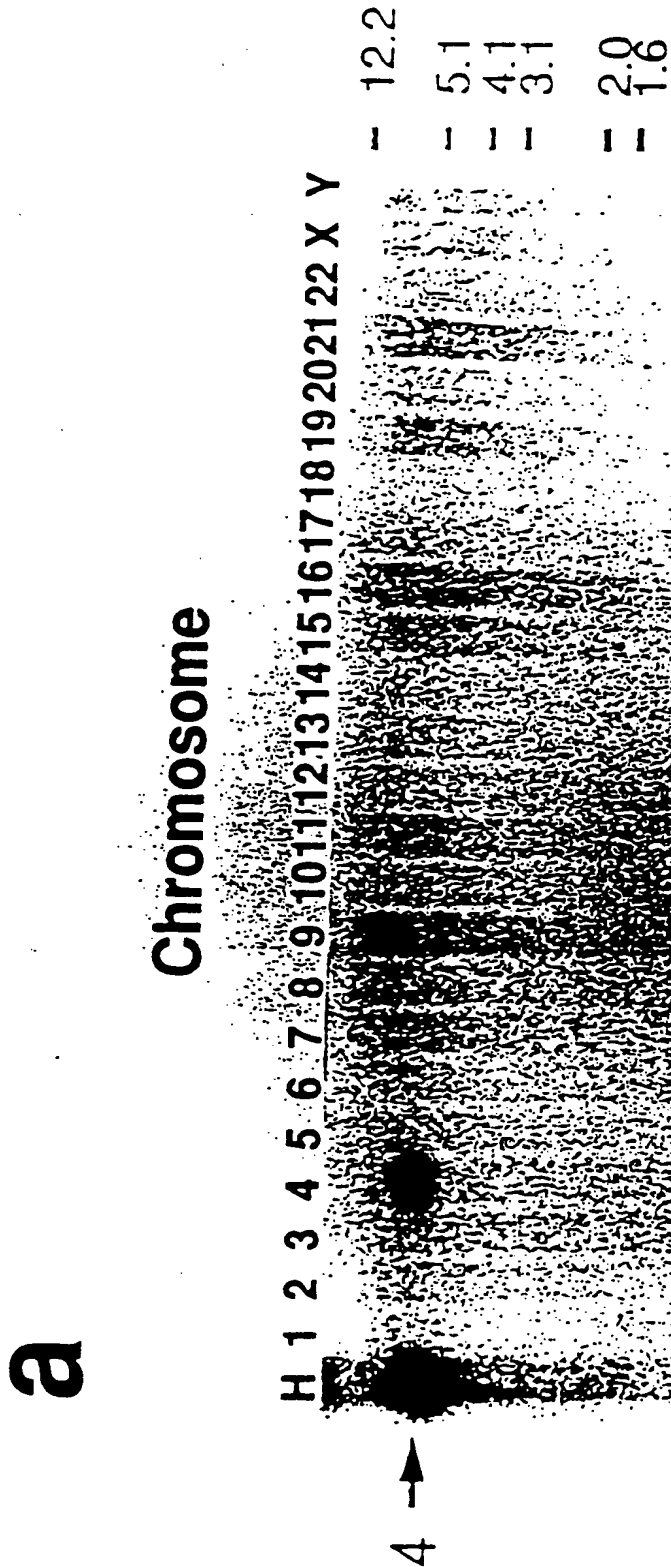


Fig. 17

b

Chromosome

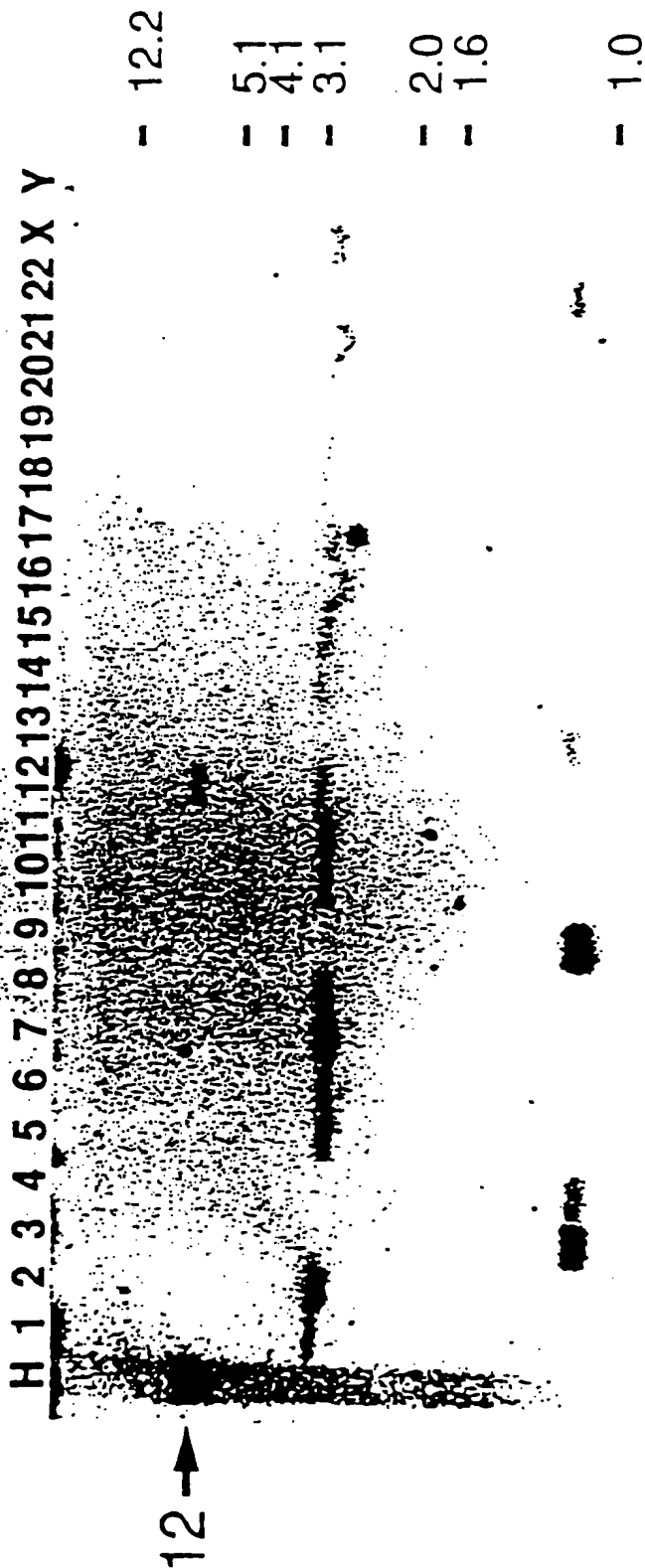


Fig. 18

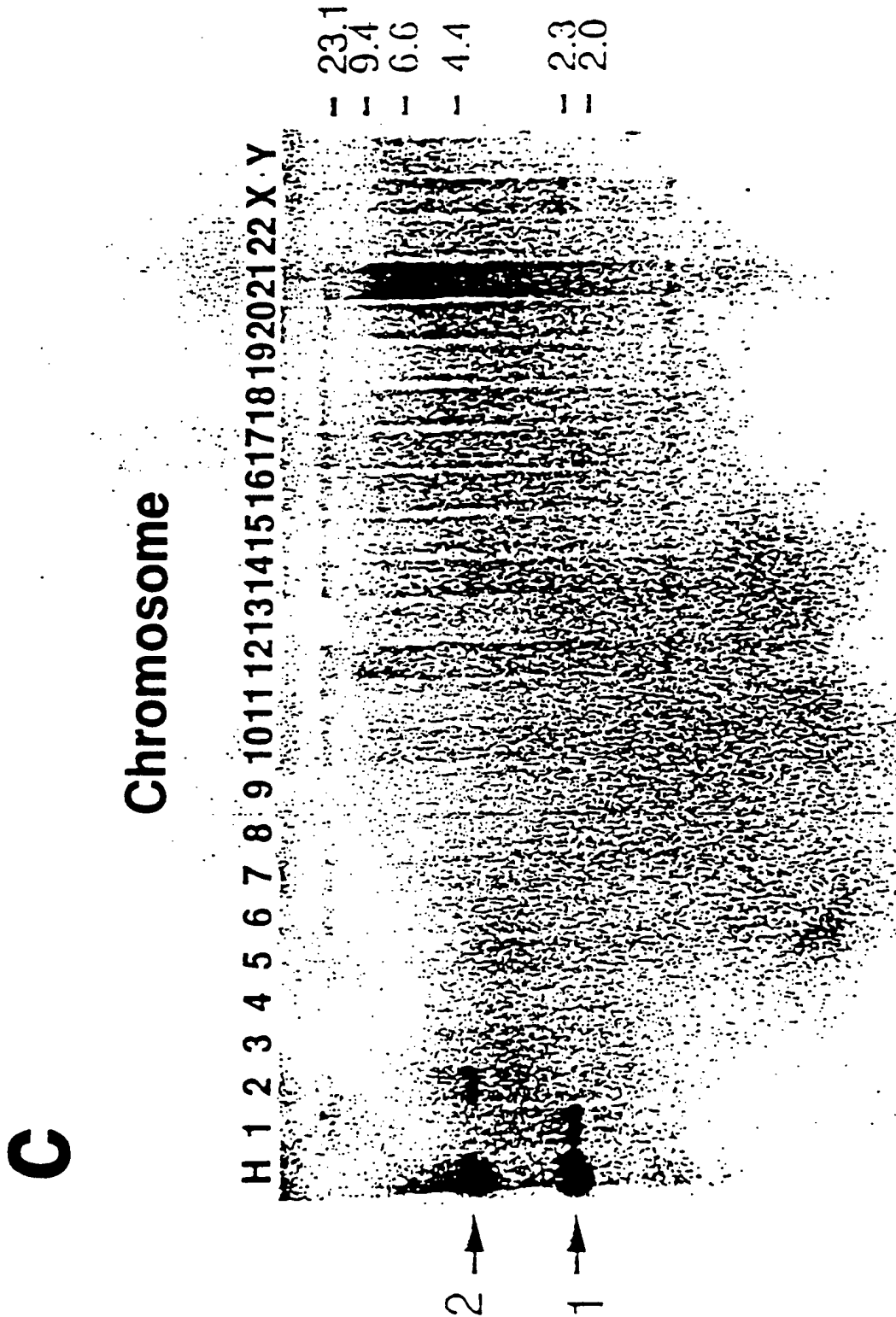


Fig. 19

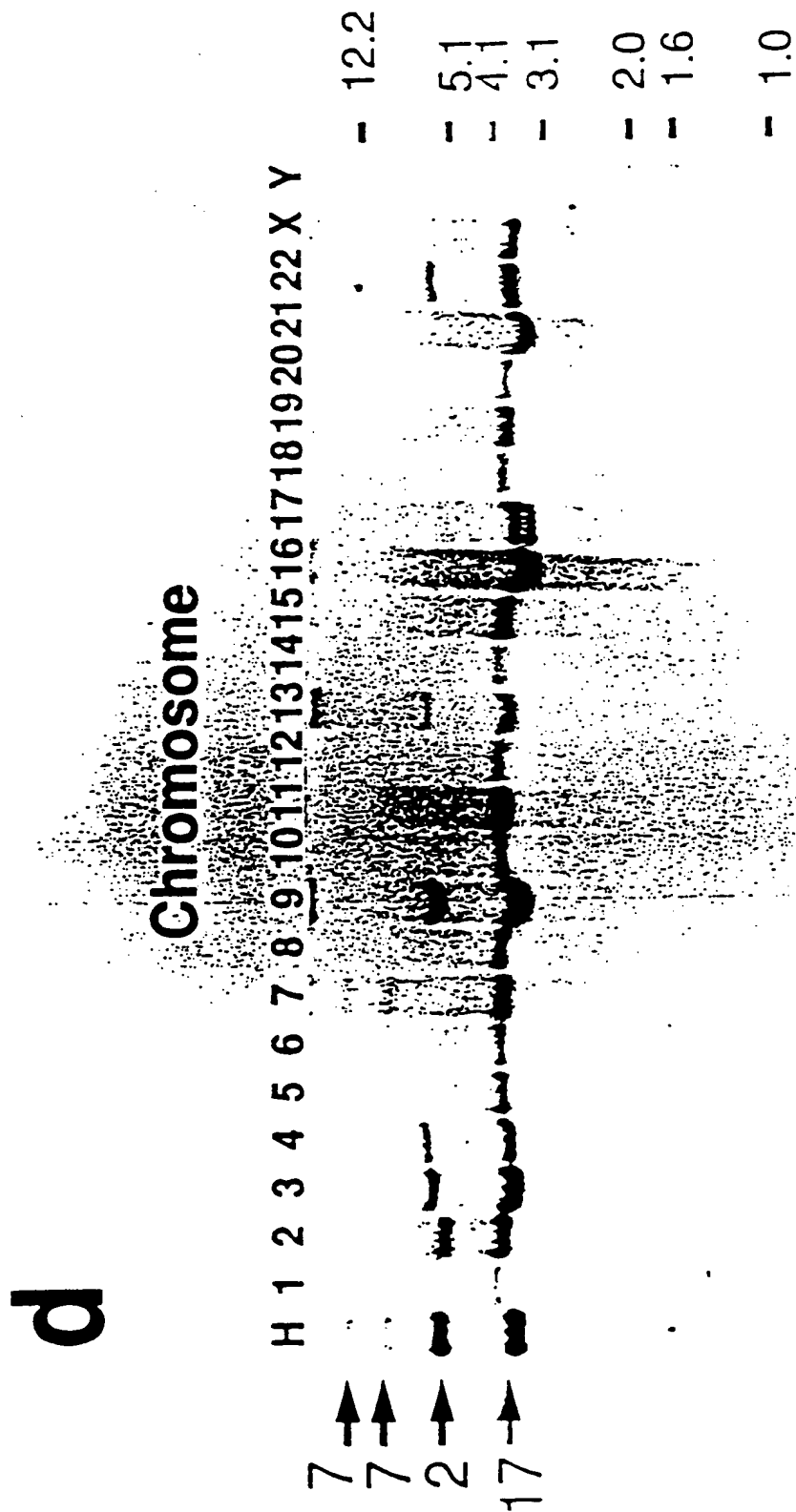


Fig. 20

e

Chromosome

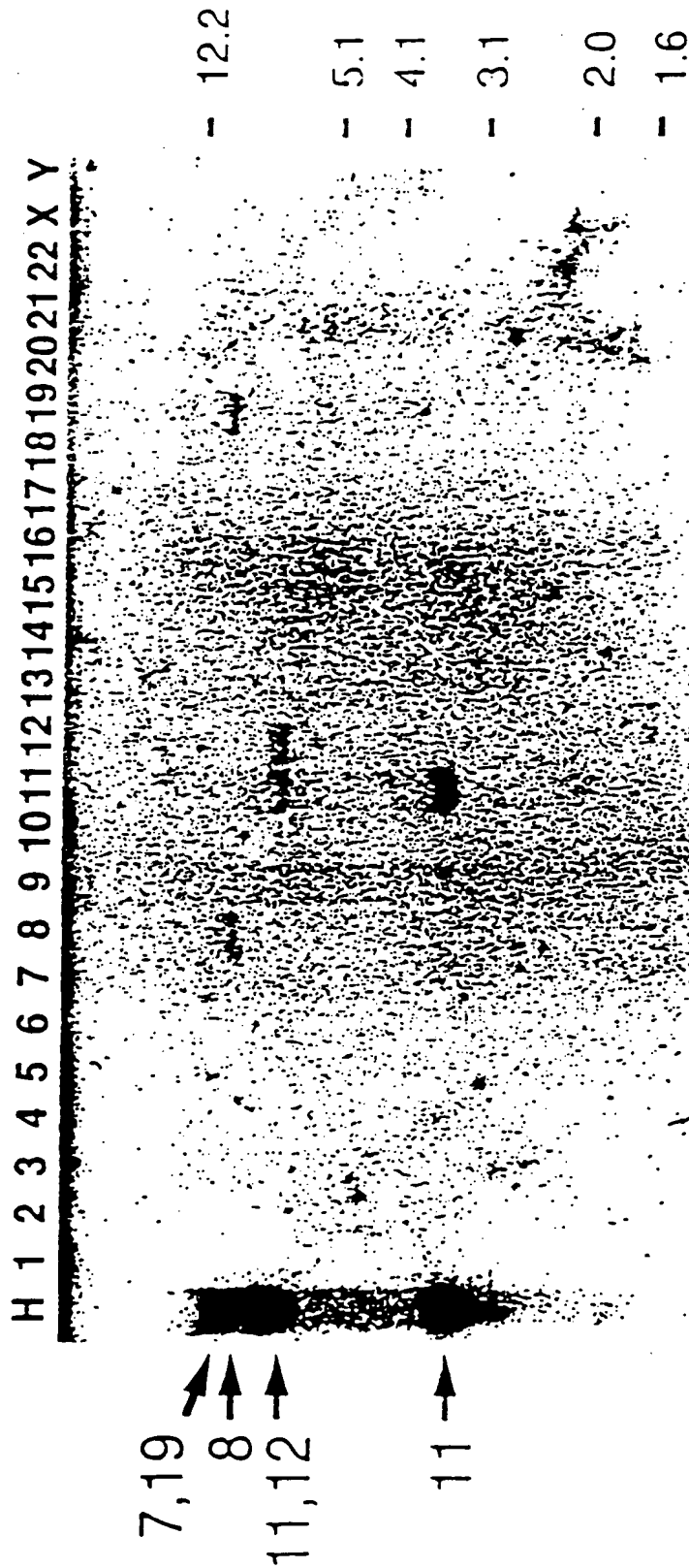


Fig. 21

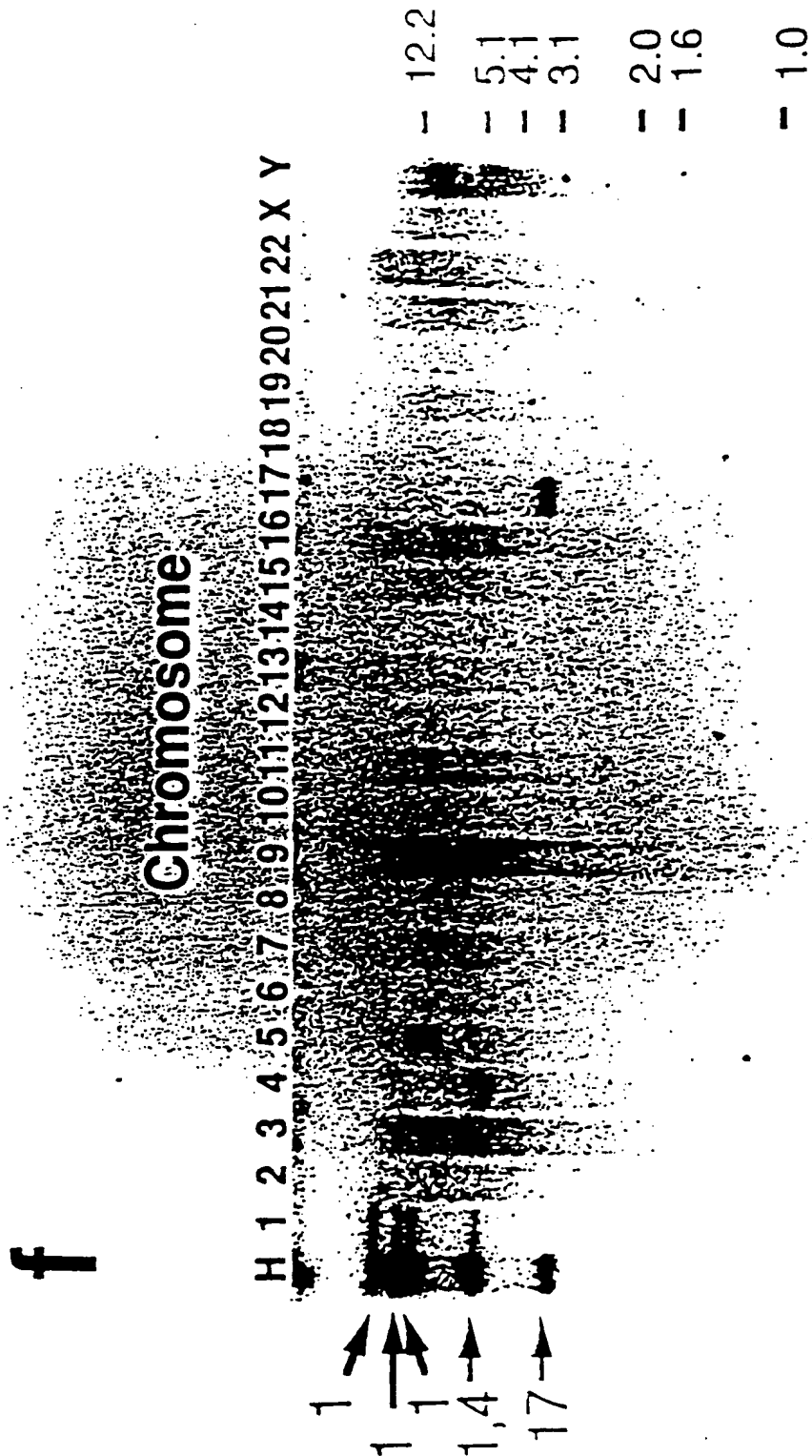


Fig. 22

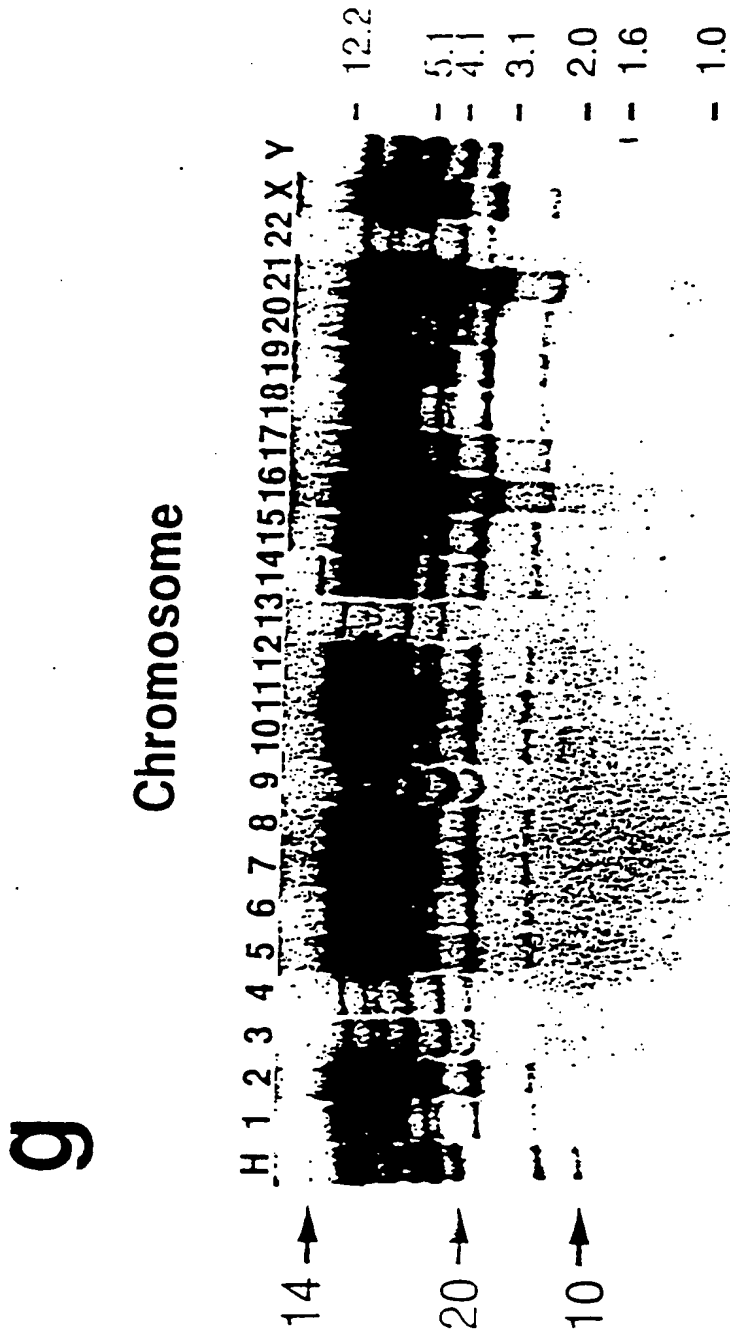


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background	
Clone	Sequence length	Ξ	Ξ/Ξ_1	Ξ/Ξ_2	Ξ_1/Ξ_2		Mouse	Chinese hamster
Single band group:								
c12e11	GS000075	432	1	1	1	9	0	0
c12e06	GS000062	540	1	1	1	6.15	0	0
c12e01	GS000290	212	1	1	1	2	1	1
c13e05	GS000117	359	1	1	1	11-	0	0
c13e07	GS000120	355	1	1	1	2	0	0
c13f10	GS000206	267	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	12-	0	0
c13h02	GS000222	167	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	3	0	0
d0h07	GS000164	313	1	1	1	11	1	1
d1b10	GS000343	153	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	27	0	0
hm01e09	GS000423	157	0	1	1	1	0	0
hm01e12	junk	394	1	1	1	17	0	0
hm01f05	GS000066	434	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	13	0	0
hm02a02	GS000130	344	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	10	0	0
hm02e01	GS000203	271	1	1	1	16	0	0
hm02e01	GS000015	590	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	14	0	0
hm02e05	GS000401	223	1	1	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	17	0	0
hm05e05	GS000251	219	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	0	0
km001	junk	169	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	5	0	0
s110	GS000057	471	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	1	7	0	0
s11h01	GS000293	204	1	1	1	3	0	0
s147	GS000050	461	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	4	1	1
s150	GS000143	330	1	1	1	17	0	0
s156	GS000002	306	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	14	0	0
s179	GS000275	196	1	1	1	n.d.	0	0
s246	GS000234	241	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	0	0
s270	junk	135	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes				Chromosomes assigned		Background			
Clone	Sequence length	±	2/3±	3/3±	3±/3±	Mouse	Chinese hamster		
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000255	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	537	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s550	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	GS000096	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group:									
c12f12	GS000195	277	1	2	2	2	1.	1	1
c13d02	GS000042	503	2	2	1	1	2.	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	3
hm01a07	GS000207	269	2	2	2	2	7.	0	0
hm01d05	GS000232	243	2	2	2	1	2.	0	0
hm01e01	GS000131	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3.	1	1
hm02c04	GS000221	253	2	2	2	2	3.	0	0
hm02e05	GS000146	332	2	2	2	2	17,19,22	0	0
hm03f07	GS000043	503	1	1	2	1	3.	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6.	0	0
s124	GS000083	404	2	2	2	2	9.	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2.	3	2
s15e02	junk	439	2	2	1	2	6.	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14.	0	0
s231	junk	284	2	2	2	2	11.	0	0
s234	GS000124	353	2	2	2	2	1.	3	1
s255	GS000235	219	2	2	2	2	11.	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B ₁	E/B ₂	B ₁ /B ₂			Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	339	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s333	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	250	1	1	1	2	9,13	0	0
s639	GS000257	205	1	2	2	2	2X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
twl-33	junk	352	2	2	2	2	1.	0	0
twl-39	GS000153	#321	2	2	2	2	17.	0	0
twl-70	GS000061	441	1	1	2	1	11.	0	0
twl-80	junk	453	2	2	1	2	9,17	2	2
twl-87	GS000158	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	373	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	131	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
twl-82	GS000203	267	3	3	3	3	13.	4	0
Four band group									
cl2g07	GS000154	320	4	4	2	3	5, 14.	0	0
cl3a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
cl3c04	GS000106	#376	4	3	3	3	n.d.	0	2
cl3e09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4X	2	1
s163	GS000004	#613	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
cl2f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	15	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X	9	8
hm01f04	GS000246	315	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	E	E/B ₁	E/B ₂	B ₁ /B ₂		Mouse	Chinese hamster	
hm02f09	GS000273	442	8	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	5	6	4	6	2,3,17.	3	3
hm05a04	GS000236	#239	6	6	6	7	n.d.	3	5
km501	junk	350	3	5	5	5	13.	14	7
s11f06	GS000315	170	6	6	6	4	1,2,2,3,4,6,13,15.	0	3
s14f01	GS000407	262	12	11	10	9	1,5,9,13.	6	3
s173	GS000094	397	5	4	6	8	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13.	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X.	3	5
tw1-63	junk	203	8	10	10	12	3,4.	17	11
Bands no detected:									
c13g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiation, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
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☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

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Name and mailing address of the ISA/

Japanese Patent Office

Authorized officer

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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
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X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
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X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al. "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
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X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
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X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

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International application No.

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
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X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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International application No.

PCT/JP94/01916

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
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X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an/ adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
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X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
X	Genomics, Vol. 4, 1989, Todd, S. et al. "cDNA sequence, interspecies comparison and gene mapping analysis of argininosuccinate lyase" p. 53-59	1-6 (3575)
X	FEBS Lett., Vol. 207, 1986, Codina, J. et al. "-Subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical" p. 187-192	1-6 (3796)
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X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

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